



## Blast 2 Sequences results

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Taxonomy

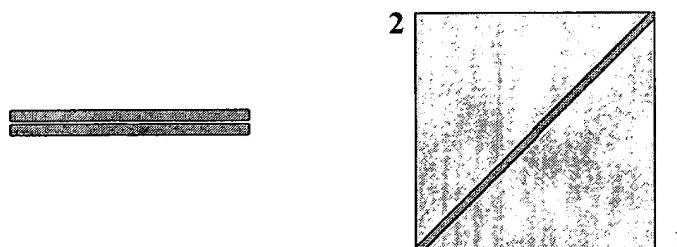
Structure

### BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.4 [Aug-26-2002]

Matrix **BLOSUM62** ▼ gap open: **11** gap extension: **1**  
x\_dropoff: **50** expect: **10.00** wordsize: **3** Filter  Align

**Sequence 1** gi 6746554 10-deacetylba<sup>c</sup>cin III-10-O-acetyl transferase [Taxus cuspidata] **Length** 440 (1 .. 440)

**Sequence 2** gi 18034655 10-deacetylba<sup>c</sup>cin III-10-O-acetyl transferase [Taxus baccata] **Length** 440 (1 .. 440)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 857 bits (2215), Expect = 0.0  
Identities = 430/440 (97%), Positives = 432/440 (97%)



Query: 1 MAGSTEFVRSLERVMVAPSQSPKAFLQLSTLDNLPGVRENIFNTLLVYNASDRVSVDP 60  
MAGSTE VVRSLERVMVAPSQSPKAFLQLSTLDNLPGVRENIFNTLLVYNASDRVSVDP

Sbjct: 1 MAGSTESVRSLERVMVAPSQSPKAFLQLSTLDNLPGVRENIFNTLLVYNASDRVSVDP 60

Query: 61 AKVIHQALSKVLVYYSPFAGRLRKENGDLVECTGEGALFVEAMADTDLSVLGDLDYS 120  
AKVIHQALSKVLVYYSPFAGRLRKENGDLVECTGEGALFVEAMADTDLSVLGDLDYS

Sbjct: 61 AKVIHQALSKVLVYYSPFAGRLRKENGDLVECTGEGALFVEAMADTDLSVLGDLDYS 120

Query: 121 PSLEQLLFCCLPPDTIEDIHPVVQVTRFTCGGFVVGVSFCHGICDGLGAGQFLIAMGEM 180  
PSLEQLLFCCLPPDTIEDIHPVVQVTRFTCGGFVVGVSFCHGICDGLGAGQFLIAMGEM

Sbjct: 121 PSLEQLLFCCLPPDTIEDIHPVVQVTRFTCGGFVVGVSFCHGICDGLGAGQFLIAMGEM 180

Query: 181 ARGEIKPSSEPIWKRELLKPEDPLYRFQYYHFQLICPPSTFGKIVQGSVLITSETINC 240  
ARGEIKPSSEPIWKRELLKPEDPLYRFQYYHF+LI PPSTFGKIVQGS 1TSETI IK

Sbjct: 181 ARGEIKPSSEPIWKRELLKPEDPLYRFQYYHFRLIRPPSTFGKIVQGS LGITSETIKWIK 240

Query: 241 QCLREESKEFCSAFEVVSALAWIARTRALQIPHSENVKLIFAMD MRKLFNPPLSKGYYGN 300  
QCLREESKEFCSAFEVVSALAWIARTRALQIPHSENVKLIFAMD MRKLFNPPL KGYYGN

Sbjct: 241 QCLREESKEFCSAFEVVSALAWIARTRALQIPHSENVKLIFAMD MRKLFNPPLKGYYGN 300

Query: 301 FVGTVCAMDNVKDLLSGSLLRVVRIIKKAKVSLNEHFTSTIVTPRSGSDESINYENIVGF 360  
FVGTVCAMDNVKDLLSGSLLRVVRIIKKAKVSLNEHFTSTIVTP SGSDESINYENIVGF

Sbjct: 301 FVGTVCAMDNVKDLLSGSLLRVVRIIKKAKVSLNEHFTSTIVTPCSGSDESINYENIVGF 360

Query: 361 GDRRLRGFDEVDFGWGHADNVSLVQHGLKDVSVVQSYFLFIRPPKNNPDGIKILSFMP 420  
GDRRLRGFDEVDFGWGHADNVSLVQHGLKDVSVVQSYFLFIRPPKNNPDGIKILSFMP

Sbjct: 361 GDRRLRGFDEVDFGWGHADNVSLVQHGLKDVSVVQSYFLFIRPPKNNPDGIKILSFMP 420

Query: 421 IVKSFKFEMETMTNKYVTKP 440  
I+KSFKFEMETMTNKYVTKP

Subjct: 421 IMKSFKFEMETMTNKYVTKP 440

CPU time: 0.08 user secs. 0.03 sys. secs 0.11 total secs.

Lambda K H  
0.321 0.139 0.414

Gapped

Lambda K H  
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 1809

Number of Sequences: 0

Number of extensions: 119

Number of successful extensions: 1

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 1

length of query: 440

length of database: 414,047,803

effective HSP length: 129

effective length of query: 311

effective length of database: 414,047,674

effective search space: 128768826614

effective search space used: 128768826614

T: 9

A: 40

X1: 16 ( 7.4 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 41 (21.9 bits)

S2: 76 (33.9 bits)